

Application  
Number

SEARCH

IDS Flag Clearance for Application 10766421

IDS  
Information

Content	Mailroom Date	Entry Number	IDS Review	Reviewer
M844	11-24-2004	16	<input checked="" type="checkbox"/>	12-16-2004 13:56:16 gtrammell
M844	01-27-2004	21	<input checked="" type="checkbox"/>	01-03-2006 07:37:32 YPak

UPDATE

## Message Display



This Action cannot be performed as there is a(n) Prior Art  
Filed action waiting for response

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Database : A\_Geneseq\_21:\*  
 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
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 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*  
 9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1298	100.0	254	4	AAB47522	Aab47522 (R)-2-oct
2	944	72.7	254	4	AAB49773	Aab49773 Protein w
3	586.5	45.2	257	7	ADF06077	Adf06077 Bacterial
4	582.5	44.9	248	6	ADB06934	Adb06934 Alloiococ
5	582.5	44.9	281	6	ADB06936	Adb06936 Alloiococ
6	574.5	44.3	246	8	ADN17584	Adn17584 Bacterial
7	505.5	38.9	261	6	ABU29919	Abu29919 Protein e
8	498.5	38.4	261	5	AAE20115	Aae20115 Lactobaci
9	496.5	38.3	261	9	ADZ77293	Adz77293 Bacillus
10	495.5	38.2	261	9	ADZ77291	Adz77291 Bacillus
11	495.5	38.2	261	9	ADZ77289	Adz77289 Bacillus
12	495.5	38.2	261	9	ADZ77283	Adz77283 Bacillus
13	494.5	38.1	261	3	AAy96271	Aay96271 B. subtil
14	494.5	38.1	261	3	AAy54424	Aay54424 Amino aci

RESULT 1

AAB47522

ID AAB47522 standard; protein; 254 AA.

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AC AAB47522;

XX

DT 04-DEC-2001 (first entry)

XX

DE (R)-2-octanol dehydrogenase.

XX

KW (R)-2-octanol dehydrogenase; ketone; alcohol; beta-NAD; co-enzyme;

KW oxidize; optical isomer; (R)-2-octanol; 4-haloacetoacetate ester;

KW (S)-4-halo-3-hydroxybutyrate ester; HMG-CoA reductase inhibitor;

KW D-carnitine; (R)-propoxybenzene.

XX

OS *Pichia finlandica*.

XX

PN WO200161014-A1.

XX

PD 23-AUG-2001.

XX

PF 15-FEB-2001; 2001WO-JP001082.

XX

PR 16-FEB-2000; 2000JP-00043506.

PR 08-DEC-2000; 2000JP-00374593.

XX

PA (DAIL ) DAICEL CHEM IND LTD.

XX

PI Kudoh M, Yamamoto H;

XX

DR WPI; 2001-596701/67.

DR N-PSDB; AAH43472.

XX

PT (R)-2-octanol dehydrogenase for producing intermediates for HMG-CoA

PT reductase inhibitors or D-carnitine.

XX

PS Claim 9; Page 83-85; 97pp; Japanese.

XX

CC This sequence represents (R)-2-octanol dehydrogenase which has the  
 CC following characteristics: (1) produces ketones by oxidizing alcohol  
 CC using beta-NAD as a co-enzyme; and produces alcohols by reducing ketones  
 CC using beta-NADH as a co-enzyme; and (2) preferentially oxidizes the  
 CC optical isomer (R)-2-octanol; and reduces 4-haloacetoacetate ester to  
 CC produce (S)-4-halo-3-hydroxybutyrate ester. (S)-4-halo-3-hydroxybutyrate  
 CC esters are useful as intermediates for HMG-CoA reductase inhibitors or D-  
 CC carnitine. (R)-propoxybenzene derivatives are particularly useful as  
 CC intermediates for optical isomers of ofloxane ((S)-(-)-9-fluoro-3-methyl-  
 CC 10-(4-methyl-1-piperazinyl)-7-oxo-2,3-dihydro-7H-pyrido(1,2,3-de)(1,4)  
 CC benzoxadin-6-carboxylic acid)

XX

SQ Sequence 254 AA;

Query Match 100.0%; Score 1298; DB 4; Length 254;

Best Local Similarity 100.0%; Pred. No. 2.9e-119;

Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSYNFHNKVAVVTGALSGIGLSVAKKFLQLGAKVTISDVSGEKKYHETTVVALKAQNLNTD 60

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Db      1 MSYNFHNKVAVVTGALSGIGLSVAKKFLQLGAKVTISDVSGEKKYHETVVALKAQNLNTD 60
Qy      61 NLHYVQADSSKEEDNKKLISETLATFGGLDIVCANAGIGKFAPTHETPPFDVWKKVIAVNL 120
Db      61 NLHYVQADSSKEEDNKKLISETLATFGGLDIVCANAGIGKFAPTHETPPFDVWKKVIAVNL 120
Qy      121 NGVFLLDKLAINYWLEKSKPGVIVNMGSVHSFVAAPGLAHYGAAGGVKLLTQTLALEYA 180
Db      121 NGVFLLDKLAINYWLEKSKPGVIVNMGSVHSFVAAPGLAHYGAAGGVKLLTQTLALEYA 180
Qy      181 SHGIRVNSVNPGYISTPLIDEVPKERLDKLVSLHPIGRLGRPEEVADAVAFLCSQEATFI 240
Db      181 SHGIRVNSVNPGYISTPLIDEVPKERLDKLVSLHPIGRLGRPEEVADAVAFLCSQEATFI 240
Qy      241 NGVSLPVDGGYTAQ 254
Db      241 NGVSLPVDGGYTAQ 254

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RESULT 2

AAB49773

ID AAB49773 standard; protein; 254 AA.

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AC AAB49773;

XX

DT 23-APR-2001 (first entry)

XX

DE Protein with acetylpyridine derivative reducing action.

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KW Optically-active pyridineethanol derivative; asymmetric reduction.

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OS Candida maris.

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PN WO200105996-A1.

XX

PD 25-JAN-2001.

XX

PF 28-JUN-2000; 2000WO-JP004237.

XX

PR 21-JUL-1999; 99JP-00206503.

XX

PA (KANF ) KANEKA CORP.

XX

PI Kawano S, Horikawa M, Yasohara Y, Hasegawa J;

XX

DR WPI; 2001-159546/16.

DR N-PSDB; AAF29375, AAF29376.

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PT Efficient, high-yielding preparation of optically-active pyridineethanol  
PT derivatives by stereoselectively reducing acetylpyridine derivatives e.g.  
PT with enzyme having asymmetric reduction activity, for pharmaceutical  
PT intermediates.

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PS Claim 14; Fig 1; 76pp; Japanese.

XX

CC This invention relates to a process for producing optically-active



Database : Issued\_Patents\_AA:\*  
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 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	1298	100.0	254	2	US-09-978-758-2	Sequence 2, Appli
2	586.5	45.2	257	2	US-09-543-681A-6362	Sequence 6362, Ap
3	503.5	38.8	309	2	US-09-248-796A-16823	Sequence 16823, A
4	494.5	38.1	261	2	US-09-468-738A-29	Sequence 29, Appl
5	494.5	38.1	261	2	US-09-940-019-29	Sequence 29, Appl
6	494.5	38.1	261	2	US-09-940-037A-29	Sequence 29, Appl
7	494.5	38.1	261	2	US-09-305-390-18	Sequence 18, Appl
8	477.5	36.8	263	2	US-09-710-279-204	Sequence 204, App
9	472.5	36.4	267	2	US-09-134-001C-5042	Sequence 5042, Ap
10	470.5	36.2	251	2	US-09-648-004-20	Sequence 20, Appl
11	470.5	36.2	251	2	US-10-272-419-20	Sequence 20, Appl
12	453.5	34.9	261	2	US-10-004-115B-36	Sequence 36, Appl
13	440	33.9	252	2	US-08-822-322-8	Sequence 8, Appli
14	440	33.9	252	2	US-09-466-109-8	Sequence 8, Appli
15	425	32.7	277	2	US-09-543-681A-8037	Sequence 8037, Ap

Database : UniProt\_05.80:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	619.5	47.7	247	2	Q81AU6_BACCR	Q81au6 bacillus ce
2	577	44.5	246	2	Q8G0H2_BRUSU	Q8g0h2 brucella su
3	511.5	39.4	262	2	Q5A1C0_CANAL	Q5a1c0 candida alb
4	504.5	38.9	262	2	Q5FK32_LACAC	Q5fk32 lactobacill
5	494.5	38.1	261	1	DHG_BACSU	P12310 bacillus su
6	491.5	37.9	261	1	DHGA_BACME	P10528 bacillus me
7	490	37.8	244	2	Q8ELC2_OCEIH	Q8elc2 oceanobacil
8	488.5	37.6	261	1	DHG4_BACME	P39485 bacillus me
9	485.5	37.4	261	2	Q632X4_BACCZ	Q632x4 bacillus ce
10	484.5	37.3	261	2	Q81KM8_BACAN	Q81km8 bacillus an
11	482.5	37.2	261	1	DHG3_BACME	P39484 bacillus me
12	478.5	36.9	261	2	Q4MVK1_BACCE	Q4mvk1 bacillus ce
13	478.5	36.9	263	2	Q5HLZ1_STAEQ	Q5hlz1 staphylococ
14	477.5	36.8	261	1	DHG2_BACME	P39483 bacillus me
15	477.5	36.8	261	2	Q6HCG4_BACHK	Q6hcg4 bacillus th
16	477.5	36.8	261	2	Q9F2A6_BACLI	Q9f2a6 bacillus li
17	477.5	36.8	261	2	Q65HM4_BACLD	Q65hm4 bacillus li
18	474.5	36.6	261	2	Q5BMD7_BACME	Q5bmd7 bacillus me
19	473.5	36.5	259	2	Q831W5_ENTFA	Q831w5 enterococcu
20	473.5	36.5	261	2	Q5BMD8_BACME	Q5bmd8 bacillus me



Database : PIR\_80:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

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# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	494.5	38.1	261	2	D69629	glucose 1-dehydrog
2	491.5	37.9	261	1	S00812	glucose 1-dehydrog
3	488.5	37.6	261	2	I40225	glucose 1-dehydrog
4	482.5	37.2	261	2	I40224	glucose 1-dehydrog
5	477.5	36.8	261	2	I39853	glucose 1-dehydrog
6	471.5	36.3	255	1	S39737	glucose 1-dehydrog
7	455.5	35.1	261	2	A33528	glucose 1-dehydrog
8	454.5	35.0	261	2	JS0385	glucose 1-dehydrog
9	448	34.5	262	2	S02299	glucose 1-dehydrog
10	448	34.5	272	2	AG3359	glucose 1-dehydrog
11	446.5	34.4	263	2	S01227	glucose 1-dehydrog
12	422.5	32.6	255	2	G82644	2,5-dichloro-2,5-c
13	420.5	32.4	258	2	G69755	glucose 1-dehydrog
14	418.5	32.2	269	2	AE2285	glucose 1-dehydrog
15	413.5	31.9	250	1	S47054	probable dehydroge
16	404.5	31.2	251	2	G72389	oxidoreductase, sh
17	396	30.5	246	2	A69621	3-oxoacyl-[acyl-ca
18	395.5	30.5	245	2	AE3517	3-oxoacyl-(acyl-ca
19	393	30.3	257	2	A72395	oxidoreductase, sh
20	391.5	30.2	271	2	AG3285	3-hydroxybutyrate